

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 10/791, 017C
Source: JFW16
Date Processed by STIC: 07/27/2006

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 07/27/2006

PATENT APPLICATION: US/10/791,017C

TIME: 09:50:25

Input Set: A:\791017eightsequences.txt

Output Set: N:\CRF4\07272006\J791017C.raw

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3 <110> APPLICANT: JENAPHARM GmbH & Co. KG
W--> 4 <120> TITLE OF INVENTION: Methods for Determining Hormonal Effects
W--> 5 of Substances
W--> 6 <130> FILE REFERENCE: Pat 3684/11
W--> 7 <140> CURRENT APPLICATION NUMBER: US/10/791,017C
8 <141> CURRENT FILING DATE: 2004-03-02
W--> 9 <160> NUMBER OF SEQ ID: 8
10 <170> SOFTWARE: PatentIn Ver. 2.1
W--> 11 <210> SEQ ID NO: 1
12 <211> LENGTH: 2390
13 <212> TYPE: DNA
14 <213> ORGANISM: Homo sapiens
W--> 15 <220> FEATURE:
16 <221> NAME/KEY: CDS
17 <222> LOCATION: (44)..(2011)
18 <223> OTHER INFORMATION: EWS
W--> 19 <400> SEQUENCE: 1
20 agaggggagac ggacgttgag agaacgagga ggaaggagag aaa atg gcg tcc acg 55
21 Met Ala Ser Thr
22 1
24 gat tac agt acc tat agc caa gct gca gcg cag cag ggc tac agt gct 103
25 Asp Tyr Ser Thr Tyr Ser Gln Ala Ala Ala Gln Gln Tyr Ser Ala
26 5 10 15 20
28 tac acc gcc cag ccc act caa gga tat gca cag acc acc cag gca tat 151
29 Tyr Thr Ala Gln Pro Thr Gln Gly Tyr Ala Gln Thr Thr Gln Ala Tyr
30 25 30 35
32 ggg caa caa agc tat gga acc tat gga cag ccc act gat gtc agc tat 199
33 Gly Gln Gln Ser Tyr Gly Thr Tyr Gly Gln Pro Thr Asp Val Ser Tyr
34 40 45 50
36 acc cag gct cag acc act gca acc tat ggg cag acc gcc tat gca act 247
37 Thr Gln Ala Gln Thr Thr Ala Thr Tyr Gly Gln Thr Ala Tyr Ala Thr
38 55 60 65
40 tct tat gga cag cct ccc act ggt tat act act cca act gcc ccc cag 295
41 Ser Tyr Gly Gln Pro Pro Thr Gly Tyr Thr Thr Pro Thr Ala Pro Gln
42 70 75 80
44 gca tac agc cag cct gtc cag ggg tat ggc act ggt gct tat gat acc 343
45 Ala Tyr Ser Gln Pro Val Gln Gly Tyr Gly Thr Gly Ala Tyr Asp Thr
46 85 90 95 100
48 acc act gct aca gtc acc acc acc cag gcc tcc tat gca gct cag tct 391
49 Thr Thr Ala Thr Val Thr Thr Thr Gln Ala Ser Tyr Ala Ala Gln Ser
50 105 110 115
52 gca tat ggc act cag cct gct tat cca gcc tat ggg cag cag cca gca 439
53 Ala Tyr Gly Thr Gln Pro Ala Tyr Pro Ala Tyr Gly Gln Gln Pro Ala

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54          120          125          130
56 gcc act gca cct aca aga ccg cag gat gga aac aag ccc act gag act 487
57 Ala Thr Ala Pro Thr Arg Pro Gln Asp Gly Asn Lys Pro Thr Glu Thr
58          135          140          145
60 agt caa cct caa tct agc aca ggg ggt tac aac cag ccc agc cta gga 535
61 Ser Gln Pro Gln Ser Ser Thr Gly Gly Tyr Asn Gln Pro Ser Leu Gly
62          150          155          160
64 tat gga cag agt aac tac agt tat ccc cag gta cct ggg agc tac ccc 583
65 Tyr Gly Gln Ser Asn Tyr Ser Tyr Pro Gln Val Pro Gly Ser Tyr Pro
66 165          170          175          180
68 atg cag cca gtc act gca cct cca tcc tac cct cct acc agc tat tcc 631
69 Met Gln Pro Val Thr Ala Pro Pro Ser Tyr Pro Pro Thr Ser Tyr Ser
70          185          190          195
72 tct aca cag ccg act agt tat gat cag agc agt tac tct cag cag aac 679
73 Ser Thr Gln Pro Thr Ser Tyr Asp Gln Ser Ser Tyr Ser Gln Gln Asn
74          200          205          210
76 acc tat ggg caa ccg agc agc tat gga cag cag agt agc tat ggt caa 727
77 Thr Tyr Gly Gln Pro Ser Ser Tyr Gly Gln Gln Ser Ser Tyr Gly Gln
78          215          220          225
80 caa agc agc tat ggg cag cag cct ccc act agt tac cca ccc caa act 775
81 Gln Ser Ser Tyr Gly Gln Gln Pro Pro Thr Ser Tyr Pro Pro Gln Thr
82          230          235          240
84 gga tcc tac agc caa gct cca agt caa tat agc caa cag agc agc agc 823
85 Gly Ser Tyr Ser Gln Ala Pro Ser Gln Tyr Ser Gln Gln Ser Ser Ser
86 245          250          255          260
88 tac ggg cag cag agt tca ttc cga cag gac cac ccc agt agc atg ggt 871
89 Tyr Gly Gln Gln Ser Ser Phe Arg Gln Asp His Pro Ser Ser Met Gly
90          265          270          275
92 gtt tat ggg cag gag tct gga gga ttt tcc gga cca gga gag aac cgg 919
93 Val Tyr Gly Gln Glu Ser Gly Gly Phe Ser Gly Pro Gly Glu Asn Arg
94          280          285          290
96 agc atg agt ggc cct gat aac cgg ggc agg gga aga ggg gga ttt gat 967
97 Ser Met Ser Gly Pro Asp Asn Arg Gly Arg Gly Arg Gly Gly Phe Asp
98          295          300          305
100 cgt gga ggc atg agc aga ggt ggg cgg gga gga gga cgc ggt gga atg 1015
101 Arg Gly Gly Met Ser Arg Gly Gly Arg Gly Gly Gly Arg Gly Gly Met
102          310          315          320
104 ggc agc gct gga gag cga ggt ggc ttc aat aag cct ggt gga ccc atg 1063
105 Gly Ser Ala Gly Glu Arg Gly Gly Phe Asn Lys Pro Gly Gly Pro Met
106 325          330          335          340
108 gat gaa gga cca gat ctt gat cta ggc cca cct gta gat cca gat gaa 1111
109 Asp Glu Gly Pro Asp Leu Asp Leu Gly Pro Pro Val Asp Pro Asp Glu
110          345          350          355
112 gac tct gac aac agt gca att tat gta caa gga tta aat gac agt gtg 1159
113 Asp Ser Asp Asn Ser Ala Ile Tyr Val Gln Gly Leu Asn Asp Ser Val
114          360          365          370
117 act cta gat gat ctg gca gac ttc ttt aag cag tgt ggg gtt gtt aag 1207
118 Thr Leu Asp Asp Leu Ala Asp Phe Phe Lys Gln Cys Gly Val Val Lys
119          375          380          385

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121	atg aac aag aga act ggg caa ccc atg atc cac atc tac ctg gac aag	1255
122	Met Asn Lys Arg Thr Gly Gln Pro Met Ile His Ile Tyr Leu Asp Lys	
123	390 395 400	
125	gaa aca gga aag ccc aaa ggc gat gcc aca gtg tcc tat gaa gac cca	1303
126	Glu Thr Gly Lys Pro Lys Gly Asp Ala Thr Val Ser Tyr Glu Asp Pro	
127	405 410 415 420	
129	ccc act gcc aag gct gcc gtg gaa tgg ttt gat ggg aaa gat ttt caa	1351
130	Pro Thr Ala Lys Ala Ala Val Glu Trp Phe Asp Gly Lys Asp Phe Gln	
131	425 430 435	
133	ggg agc aaa ctt aaa gtc tcc ctt gct cgg aag aag cct cca atg aac	1399
134	Gly Ser Lys Leu Lys Val Ser Leu Ala Arg Lys Lys Pro Pro Met Asn	
135	440 445 450	
137	agt atg cgg ggt ggt ctg cca ccc cgt gag ggc aga ggc atg cca cca	1447
138	Ser Met Arg Gly Gly Leu Pro Pro Arg Glu Gly Arg Gly Met Pro Pro	
139	455 460 465	
141	cca ctc cgt gga ggt cca gga ggc cca gga ggt cct ggg gga ccc atg	1495
142	Pro Leu Arg Gly Gly Pro Gly Gly Pro Gly Gly Pro Gly Gly Pro Met	
143	470 475 480	
145	ggt cgc atg gga ggc cgt gga gga gat aga gga ggc ttc cct cca aga	1543
146	Gly Arg Met Gly Gly Arg Gly Gly Asp Arg Gly Gly Phe Pro Pro Arg	
147	485 490 495 500	
149	gga ccc cgg ggt tcc cga ggg aac ccc tct gga gga gga aac gtc cag	1591
150	Gly Pro Arg Gly Ser Arg Gly Asn Pro Ser Gly Gly Gly Asn Val Gln	
151	505 510 515	
153	cac cga gct gga gac tgg cag tgt ccc aat ccg ggt tgt gga aac cag	1639
154	His Arg Ala Gly Asp Trp Gln Cys Pro Asn Pro Gly Cys Gly Asn Gln	
155	520 525 530	
157	aac ttc gcc tgg aga aca gag tgc aac cag tgt aag gcc cca aag cct	1687
158	Asn Phe Ala Trp Arg Thr Glu Cys Asn Gln Cys Lys Ala Pro Lys Pro	
159	535 540 545	
161	gaa ggc ttc ctc ccg cca ccc ttt ccg ccc ccg ggt ggt gat cgt ggc	1735
162	Glu Gly Phe Leu Pro Pro Pro Phe Pro Pro Pro Gly Gly Asp Arg Gly	
163	550 555 560	
165	aga ggt ggc cct ggt ggc atg cgg gga gga aga ggt ggc ctc atg gat	1783
166	Arg Gly Gly Pro Gly Gly Met Arg Gly Gly Arg Gly Gly Leu Met Asp	
167	565 570 575 580	
169	cgt ggt ggt ccc ggt gga atg ttc aga ggt ggc cgt ggt gga gac aga	1831
170	Arg Gly Gly Pro Gly Gly Met Phe Arg Gly Gly Arg Gly Gly Asp Arg	
171	585 590 595	
173	ggt ggc ttc cgt ggt ggc cgg ggc atg gac cga ggt ggc ttt ggt gga	1879
174	Gly Gly Phe Arg Gly Gly Arg Gly Met Asp Arg Gly Gly Phe Gly Gly	
175	600 605 610	
177	gga aga cga ggt ggc cct ggg ggg ccc cct gga cct ttg atg gaa cag	1927
178	Gly Arg Arg Gly Gly Pro Gly Gly Pro Pro Gly Pro Leu Met Glu Gln	
179	615 620 625	
181	atg gga gga aga aga gga gga cgt gga gga cct gga aaa atg gat aaa	1975
182	Met Gly Gly Arg Arg Gly Gly Arg Gly Gly Pro Gly Lys Met Asp Lys	
183	630 635 640	
185	ggc gag cac cgt cag gag cgc aga gat cgg ccc tac tagatgcaga	2021

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186 Gly Glu His Arg Gln Glu Arg Arg Asp Arg Pro Tyr
187 645                      650                      655
189 gaccccgag agctgcattg actaccagat ttatttttta aaccagaaaa tgttttaaat 2081
191 ttataattcc atatttataa tgttggccac aacattatga ttattccttg tctgtacttt 2141
193 agtatttttc accatttgtg aagaaacatt aaaacaagtt aaatggtagt gtgcggagtt 2201
195 tttttttctt ctttctttta aaaatgggtt tttaagactt taacaatggg aacccttgt 2261
197 gagcatgctc agtatcattg tggagaacca agaaggcctc ttaactgtaa caatgttcat 2321
199 gggtgtgatg tttttttttt ttttttaaaa taaaattcca aatgtttaat aaaaaaaaaa 2381
201 aaaaaaaaaa                                     2390
204 <210> SEQ ID NO: 2
205 <211> LENGTH: 656
206 <212> TYPE: PRT
207 <213> ORGANISM: Homo sapiens
209 <400> SEQUENCE: 2
211 Met Ala Ser Thr Asp Tyr Ser Thr Tyr Ser Gln Ala Ala Ala Gln Gln
212 1                      5                      10                      15
214 Gly Tyr Ser Ala Tyr Thr Ala Gln Pro Thr Gln Gly Tyr Ala Gln Thr
215 20                      25                      30
217 Thr Gln Ala Tyr Gly Gln Gln Ser Tyr Gly Thr Tyr Gly Gln Pro Thr
218 35                      40                      45
220 Asp Val Ser Tyr Thr Gln Ala Gln Thr Thr Ala Thr Tyr Gly Gln Thr
221 50                      55                      60
223 Ala Tyr Ala Thr Ser Tyr Gly Gln Pro Pro Thr Gly Tyr Thr Thr Pro
224 65                      70                      75                      80
226 Thr Ala Pro Gln Ala Tyr Ser Gln Pro Val Gln Gly Tyr Gly Thr Gly
227 85                      90                      95
229 Ala Tyr Asp Thr Thr Thr Ala Thr Val Thr Thr Thr Gln Ala Ser Tyr
230 100                     105                     110
232 Ala Ala Gln Ser Ala Tyr Gly Thr Gln Pro Ala Tyr Pro Ala Tyr Gly
233 115                     120                     125
235 Gln Gln Pro Ala Ala Thr Ala Pro Thr Arg Pro Gln Asp Gly Asn Lys
236 130                     135                     140
238 Pro Thr Glu Thr Ser Gln Pro Gln Ser Ser Thr Gly Gly Tyr Asn Gln
239 145                     150                     155                     160
241 Pro Ser Leu Gly Tyr Gly Gln Ser Asn Tyr Ser Tyr Pro Gln Val Pro
242 165                     170                     175
244 Gly Ser Tyr Pro Met Gln Pro Val Thr Ala Pro Pro Ser Tyr Pro Pro
245 180                     185                     190
247 Thr Ser Tyr Ser Ser Thr Gln Pro Thr Ser Tyr Asp Gln Ser Ser Tyr
248 195                     200                     205
250 Ser Gln Gln Asn Thr Tyr Gly Gln Pro Ser Ser Tyr Gly Gln Gln Ser
251 210                     215                     220
253 Ser Tyr Gly Gln Gln Ser Ser Tyr Gly Gln Gln Pro Pro Thr Ser Tyr
254 225                     230                     235                     240
256 Pro Pro Gln Thr Gly Ser Tyr Ser Gln Ala Pro Ser Gln Tyr Ser Gln
257 245                     250                     255
259 Gln Ser Ser Ser Tyr Gly Gln Gln Ser Ser Phe Arg Gln Asp His Pro
260 260                     265                     270
262 Ser Ser Met Gly Val Tyr Gly Gln Glu Ser Gly Gly Phe Ser Gly Pro

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```

263          275          280          285
265 Gly Glu Asn Arg Ser Met Ser Gly Pro Asp Asn Arg Gly Arg Gly Arg
266          290          295          300
268 Gly Gly Phe Asp Arg Gly Gly Met Ser Arg Gly Gly Arg Gly Gly Gly
269 305          310          315          320
271 Arg Gly Gly Met Gly Ser Ala Gly Glu Arg Gly Gly Phe Asn Lys Pro
272          325          330          335
274 Gly Gly Pro Met Asp Glu Gly Pro Asp Leu Asp Leu Gly Pro Pro Val
275          340          345          350
277 Asp Pro Asp Glu Asp Ser Asp Asn Ser Ala Ile Tyr Val Gln Gly Leu
278          355          360          365
280 Asn Asp Ser Val Thr Leu Asp Asp Leu Ala Asp Phe Phe Lys Gln Cys
281          370          375          380
283 Gly Val Val Lys Met Asn Lys Arg Thr Gly Gln Pro Met Ile His Ile
284 385          390          395          400
286 Tyr Leu Asp Lys Glu Thr Gly Lys Pro Lys Gly Asp Ala Thr Val Ser
287          405          410          415
289 Tyr Glu Asp Pro Pro Thr Ala Lys Ala Ala Val Glu Trp Phe Asp Gly
290          420          425          430
292 Lys Asp Phe Gln Gly Ser Lys Leu Lys Val Ser Leu Ala Arg Lys Lys
293          435          440          445
295 Pro Pro Met Asn Ser Met Arg Gly Gly Leu Pro Pro Arg Glu Gly Arg
296          450          455          460
298 Gly Met Pro Pro Pro Leu Arg Gly Gly Pro Gly Gly Pro Gly Gly Pro
299 465          470          475          480
301 Gly Gly Pro Met Gly Arg Met Gly Gly Arg Gly Gly Asp Arg Gly Gly
302          485          490          495
304 Phe Pro Pro Arg Gly Pro Arg Gly Ser Arg Gly Asn Pro Ser Gly Gly
305          500          505          510
307 Gly Asn Val Gln His Arg Ala Gly Asp Trp Gln Cys Pro Asn Pro Gly
308          515          520          525
310 Cys Gly Asn Gln Asn Phe Ala Trp Arg Thr Glu Cys Asn Gln Cys Lys
311          530          535          540
313 Ala Pro Lys Pro Glu Gly Phe Leu Pro Pro Pro Phe Pro Pro Pro Gly
314 545          550          555          560
316 Gly Asp Arg Gly Arg Gly Gly Pro Gly Gly Met Arg Gly Gly Arg Gly
317          565          570          575
319 Gly Leu Met Asp Arg Gly Gly Pro Gly Gly Met Phe Arg Gly Gly Arg
320          580          585          590
322 Gly Gly Asp Arg Gly Gly Phe Arg Gly Gly Arg Gly Met Asp Arg Gly
323          595          600          605
325 Gly Phe Gly Gly Gly Arg Arg Gly Gly Pro Gly Gly Pro Pro Gly Pro
326          610          615          620
328 Leu Met Glu Gln Met Gly Gly Arg Arg Gly Gly Arg Gly Gly Pro Gly
329 625          630          635          640
331 Lys Met Asp Lys Gly Glu His Arg Gln Glu Arg Arg Asp Arg Pro Tyr
332          645          650          655
335 <210> SEQ ID NO: 3
336 <211> LENGTH: 20

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VERIFICATION SUMMARY

DATE: 07/27/2006

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TIME: 09:50:26

Input Set : A:\791017eightsequences.txt

Output Set: N:\CRF4\07272006\J791017C.raw

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L:6 M:283 W: Missing Blank Line separator, <130> field identifier
L:7 M:283 W: Missing Blank Line separator, <140> field identifier
L:9 M:283 W: Missing Blank Line separator, <160> field identifier
L:11 M:283 W: Missing Blank Line separator, <210> field identifier
L:15 M:283 W: Missing Blank Line separator, <220> field identifier
L:19 M:283 W: Missing Blank Line separator, <400> field identifier